Aftorney's Docket No.: 07039-298001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

pplicant: Stephen James Russell et al.

Art Unit : 1632

Serial No.: 09/667,947

Examiner: Shin-Lin Chen

Filed

: September 22, 2000

Title

THERAPEUTIC METHODS AND COMPOSITIONS USING VIRUSES OF THE

RECOMBINANT PARAMYXOVIRIDAE FAMILY

RECEIVED

MAIL STOP SEQUENCE

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

MAY 2, 8 2003

TECH CENTER 1600/2900

TRANSMITTAL LETTER

The following correspondence relating to this application is enclosed:

- 1. Response to Notice to Comply (2 pages);
- 2. Copy of Notice to Comply (10 pages);
- Paper Copy of Substitute Sequence Listing (10 pages); 3.
- Verified Statement Under 37 CFR § 1.821(f); 4.
- Computer Readable Diskette; and 5.
- Post card. 6.

Please apply any charges not covered, or any credits, to Deposit Account No. 06-1050.

Respectfully submitted,

Monica McCormick Graham, Ph.D.

Reg. No. 42,600

Fish & Richardson P.C., P.A. 60 South Sixth Street

Suite 3300

Minneapolis, MN 55402 Telephone: (612) 335-5070 Facsimile: (612) 288-9696

60142250.doc

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

May 20, 2003

Wasekus

Date of Deposit

Signature

Judith A. Wasilkus

Typed or Printed Name of Person Signing Certificate

AF/1632

Attorney's Docket No.: 07039-298001



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

plicant: Stephen James Russell et al.

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Alexandria, VA 22313-1450

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MAY 2: 9 2003

TECH CENTER 1600/2900

TRANSMITTAL LETTER

The following correspondence relating to this application is enclosed:

- 1. Amendment and Response to Office Action mailed February 20, 2003 (8 pages);
- 2. Copy of Peng et al., Nature Medicine article (5 pages);
- 3. Copy of Peng et al., Cancer Research article (7 pages); and
- 4. Post card.

Please apply any charges not covered, or any credits, to Deposit Account No. 06-1050.

Respectfully submitted,

Date: 5/20/03

Monica McCormick Graham, Ph.D.

Reg. No. 42,600

Fish & Richardson P.C., P.A. 60 South Sixth Street

Suite 3300

Minneapolis, MN 55402 Telephone: (612) 335-5070 Facsimile: (612) 288-9696

.60142268.doc

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I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Date of Deposit

Signature

Judith A. Wasilkus

Typed or Printed Name of Person Signing Certificate

Attorney's Docket No.: 07039-29800

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Stephen James Russell et al.

Art Unit : 1632

TECH CENTER 1600/2900

Serial No.: 09/667,947

Examiner: Shin-Lin Chen

Filed

September 22, 2000

Title

: THERAPEUTIC METHODS AND COMPOSITIONS USING VIRUSES OF THE

RECOMBINANT PARAMYXOVIRIDAE FAMILY

MAIL STOP SEQUENCE

Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCES

In response to the communication dated February 20, 2003 (copy enclosed), Applicants submit herewith a Sequence Listing in computer readable form as required by 37 CFR §1.824. In addition, Applicants submit a substitute Sequence Listing as required under 37 CFR §1.823(a) and a statement under 37 CFR §1.821(f). In the substitute sequence listing, the <213> section recites "artificial sequence" in place of "fragment." The substitute specification also provides the information for the <220> and <223> sections. No new matter has been introduced.

Applicants respectfully request entry of the substitute paper copy and computer readable copy of the Sequence Listing filed herewith in the instant application.

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

	May 20, 2003	
Date of Deposit	Que114/2/12	1

Signature

Judith A. Wasilkus

Typed or Printed Name of Person Signing Certificate

Applicant: Stephen James Russell et al.

Serial No.: 09/667,947

Filed : September 22, 2000

Page : 2 of 2

Please apply any charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: 5/20/03

Monica McCormick Graham, Ph.D.

Attorney's Docket No.: 07039-298001

Reg. No. 42,600

Fish & Richardson P.C., P.A. 60 South Sixth Street Suite 3300

Minneapolis, MN 55402 Telephone: (612) 335-5070 Facsimile: (612) 288-9696

60142192.doc

Application No.: 09/667, 947

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTICE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

	3	. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
Ø	4	A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
	5.	The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
	6.	The paper copy of the "Sequence Listing" is not the same as the computer reada "Sequence Listing" as required by 37 C.F.R. 1.821(e).
\Box	7	Other: MAY 2 8 2003

TECH CENTER 1600/2900

Applicant Must Provide:

An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

Patentin Software Program Support

T chnical Assistance......703-287-0200

To Purchase Patentin Software......703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAWSEQUENOCEDISTING



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: COUGA 947. RECEIVED
Source: 600
Date Processed by STIC: 016712003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRE SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER 703-308-2212

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX. 703-308-4216

PATENTIN 2:1 e-mail help: patin21help@uspto:gov.or phone 703-306-4119 (R. Ward)

PATENTIN 3:0 e-mail help: patin3help@uspto:gov.or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- | EFS-Bio (| EFS Submission | User-Manual-ePAVE|
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
 - U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
 - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1803, Crystal Plaza (1905) 2011 South Clark Place, Arlington, VA 22202
- 4. Pederal Express, United Parcel Service, or other delivery service t: U.S. Patent and Trademark Office,
 Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Carlot and particular property

Revised 01/29/2002

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHIICH WERE INSERTED BY PTO SOFTW If wrapped Mucleics Wrapped Amino Wrapped Amino The numbericat at the end of each line "wrapped" down to the next line. This may occur if your file was retired in a word processor after creating it. Please adjust your right margin to .3; this will proven the was retired in a word processor after creating it. Please adjust your right margin to .3; this will proven the was retired in a word processor after creating it. Please adjust your right margin to .3; this will proven the was retired in a word processor after creating it. Please adjust your right margin to .3; this will proven the was retired in a word processor after creating it. Please adjust your right margin to .3; this will prove the waste of the creating the provent of the submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent animal angle restlue. Please present the martinum number of each residue having variable length and indicate in the <pre></pre>	ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/667,947
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR
Misaligned Amino Numbering The numbering under each 5° amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.		was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
Numbering Numbering	2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
Sequence(s)	 -	
each nor Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220><223> section that some may be missing. A "bug" in Patentla version 2.0 has caused the <230><220> section to be missing from amino acid sequence. Please manually copy the relevant <220><223> section to the subsequent amino acid sequence. Please manually copy the relevant <220><223> section to the subsequent amino acid sequence. This applies to the mandatory <220><223> sections for Artificial or Unknown sequences. Sequence(s)	4Non-ASCII	· · · · · · · · · · · · · · · · · · ·
"bug" sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220><223> section to the subsequent amino acid sequence. This applies to the mandatory <220><223> sections for Artificial or Unknown sequences. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	5Variable Length (1971)	each n or Xaa can only represent a single resiJue. Please present the maximum number of each
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences. Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. (NEW RULES) Use of n'a or Xaa's (NEW RULES) Use of n'a and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. Misuse of n		sequences(s) Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Skipped Sequences (NEW RULES) Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. 210> sequence id number 400> sequence id number 600 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220> <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Per 1.823 of Sequence Rules, the only valld <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220> <223> section is required when <213> response is Unknown or is Artificial Sequence Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent		(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
Vise of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220> <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.		Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Per 1.823 of Sequence Rules, the only valld <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence Use of <220>		<210> sequence id number <400> sequence id number
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence 1 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) 2 Patentln 2.0 "bug" Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. 3 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent	(NEW RULES)	Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
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"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. 3 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent		Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
	"bug"	resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence

AMC/MH - Biotechnology Systems Branch - 08/21/2001



-ombiy in Neader 140C

```
RAW SEQUENCE LISTING
                                        DATE: 01/07/2003
PATENT APPLICATION: US/09/667,947
                                       TIME: 16:31:43
Input Set : A:\07039-298001.txt
```

```
4 <110> APPLICANT: Russell, Stephen James
              Cattaneo, Roberto
              Peng, Kah-Whye
              Schneider, Urs
              Murphy, Anthea L.
     10 <120> TITLE OF INVENTION: Therapeutic methods and compositions
              using viruses of the recombinant palamyxoviridae family
     14 <130> FILE REFERENCE: 07039-298001
     16 <140> CURRENT APPLICATION NUMBER: US 09/667,947
C--> 17 <141> CURRENT FILING DATE: 2002-12-18
     19 <150> PRIOR APPLICATION NUMBER: US 60/155,873
     20 <151> PRIOR FILING DATE: 1999-09-24
     22 <160> NUMBER OF SEQ ID NOS: 49
     24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     26 <210> SEQ ID NO: 1
                                      - invalid response see error summary sheet
     27 <211> LENGTH: 4
     28 <212> TYPE: PRT
     29 <213> ORGANISM: (Fragment
                                           item 10
     31 <400> SEQUENCE: 1
     32 Ile Glu Gly Arg
     33 1
                                                        The type of errors shown exist throughout
     35 <210> SEQ ID NO: 2
                                                        the Sequence Listing. Please check subsequent
     36 <211> LENGTH: 4
                                                        sequences for similar errors
     37 <212> TYPE: PRT
     38 <213> ORGANISM: (Fragment
     40 <220> FEATURE:
     41 <221> NAME/KEY: VARIANT
     42 <222> LOCATION: 2
     43 <223> OTHER INFORMATION: Xaa = Any 20 amino acids
     45 <400> SEQUENCE: 2
W--> 46 Arg Xaa Lys Arg
    47 1
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     50 <211> LENGTH: 6
     51 <212> TYPE: PRT
     52 <213> ORGANISM: Fragment
     54 <400> SEQUENCE: 3
     55 Pro Leu Gly Leu Trp Ala
     56 1
     58 <210> SEQ ID NO: 4
     59 <211> LENGTH: 6
     60 <212> TYPE: PRT
     61 <213> ORGANISM: Fragment
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003 TIME: 16:31:43

Input Set : A:\07039-298001.txt

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63 <400> SEQUENCE: 4
64 Tyr Glu Val Asp Gly Trp
65 1
67 <210> SEQ ID NO: 5
68 <211> LENGTH: 7
69 <212> TYPE: PRT ~
70 <213> ORGANISM: \Fragment
72 <400> SEQUENCE: 5
73 Val Asp Val Ala Asp Gly Trp
74 1
76 <210> SEQ ID NO: 6
77 <211> LENGTH: 7
78 <212> TYPE: PRT,
79 <213> ORGANISM: \Fragment
81 <400> SEQUENCE: 6
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85 <210> SEQ ID NO: 7
86 <211> LENGTH: 6
87 <212> TYPE: PRT
88 <213> ORGANISM: Fragment
90 <400> SEQUENCE: 7
91 Leu Glu Val Asp Gly Trp
92 1
94 <210> SEQ ID NO: 8
95 <211> LENGTH: 6
96 <212> TYPE: PRT
97 <213> ORGANISM: Fragment
99 <400> SEQUENCE: 8
100 Val Gln Val Asp Gly Trp
        . 5
101 1
103 <210> SEQ ID NO: 9
104 <211> LENGTH: 7
105 <212> TYPE: PRT
106 <213> ORGANISM: (Fragment)
108 <400> SEQUENCE: 9
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110 1
112 <210> SEQ ID NO: 10
113 <211> LENGTH: 4
114 <212> TYPE: PRT
115 <213> ORGANISM: Fragment
117 <400> SEQUENCE: 10 .....
118 Arg Gly Leu Thr
119 1
121 <210> SEQ ID NO: 11
122 <211> LENGTH: 17
123 <212> TYPE: PRT
124 <213> ORGANISM: \sqrt{F} ragment
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RAW SEQUENCE LISTINGPATENT APPLICATION: **US/09/667,947**DATE: 01/07/2003 TIME: 16:31:43

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\1667947.raw

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126 <400> SEQUENCE: 11
 127 Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
                                         10
 128 1
 129 Pro
 132 <210> SEQ ID NO: 12
 133 <211> LENGTH: 34
 134 <212> TYPE: PRT
135 <213> ORGANISM: Fragment /
 137 <400> SEQUENCE: 12
 138 Met Ser Pro Gln Arg Asp Arg Ile Asn Ala Phe Tyr Lys Asp Asn Pro
             5
                                         10
 140 His Pro Lys Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile
 141
 142 Asp Arg
 145 <210> SEQ ID NO: 13
 146 <211> LENGTH: 33
 147 <212> TYPE: PRT
 148 <213> ORGANISM: Fragment
 150 <400> SEQUENCE: 13
 151 Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser Arg Pro
                     5
                                         10
 153 Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser
 154
 155 Leu
 158 <210> SEQ ID NO: 14
 159 <211> LENGTH: 5
 160 <212> TYPE: PRT
 161 <213> ORGANISM: Fragment /
 163 <400> SEQUENCE: 14
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 165 1
 167 <210> SEQ ID NO: 15
 168 <211> LENGTH: 4
 169 <212> TYPE: PRT
 170 <213> ORGANISM: Fragment
 172 <400> SEQUENCE: 15
 173 Arg His Lys Arg
 174 1
 176 <210> SEQ ID NO: 16
 177 <211> LENGTH: 47
 178 <212> TYPE: DNA
 179 <213> ORGANISM: Artificial Sequence
 181 <220> FEATURE:
 182 <223> OTHER INFORMATION: Primer
 184 <400> SEQUENCE: 16
 185 ttttcctttt gcggccgctt tcatcaacgc ttctgcaggg acccctc
 187 <210> SEQ ID NO: 17
 188 <211> LENGTH: 56
 189 <212> TYPE: DNA
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47

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947 TI

DATE: 01/07/2003 TIME: 16:31:43

Input Set : A:\07039-298001.txt

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190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Primer
195 <400> SEQUENCE: 17
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198 <210> SEQ ID NO: 18
199 <211> LENGTH: 18
200 <212> TYPE: PRT
201 <213> ORGANISM: Fragment
203 <400> SEQUENCE: 18
204 Val His Ala Ala Gln Pro Ala Arg Leu Lys Arg Glu Ala Glu Asp Leu
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205 1
206 Gln Val
209 <210> SEQ ID NO: 19
210 <211> LENGTH: 50
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Primer
217 <400> SEQUENCE: 19
218 ttttcctttt gcggccgctt tcatcatcaa cgcttctgca gggacccctc
                                                                           50
220 <210> SEQ ID NO: 20
221 <211> LENGTH: 59
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Primer
228 <400> SEQUENCE: 20
229 gtccatgcgg cccagccggc cggtggaggc ggttcagagg cagaggacct gcaggtggg
231 <210> SEQ ID NO: 21
232 <211> LENGTH: 19
233 <212> TYPE: PRT
234 <213> ORGANISM: Fragment /
236 <400> SEQUENCE: 21
237 Val His Ala Ala Gln Pro Ala Gly Gly Gly Ser Glu Ala Glu Asp
238 1
                     5
239 Leu Gln Val
242 <210> SEQ ID NO: 22
243 <211> LENGTH: 16
244 <212> TYPE: PRT
245 <213> ORGANISM: Fragment /
247 <400> SEQUENCE: 22
248 Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Gly Met Ser Arg Pro Gly
           5
                                        10
249 1
251 <210> SEQ ID NO: 23
252 <211> LENGTH: 9
253 <212> TYPE: PRT
254 <213> ORGANISM: Fragment
256 <400> SEQUENCE: 23
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DATE: 01/07/2003

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947 TIME: 16:31:43

Input Set : A:\07039-298001.txt

257 Arg Gly Arg Cys Asn Lys Lys Gly Glu 258 1 5	
258 1 5 260 <210> SEQ ID NO: 24	
261 <211> LENGTH: 26	
262 <212> TYPE: DNA	
263 <213> ORGANISM: Artificial Sequence	
265 <220> FEATURE:	
266 <223> OTHER INFORMATION: Primer	
268 <400> SEQUENCE: 24	
269 aaaactgcag actcaaaggt caatgc	26
271 <210> SEQ ID NO: 25	
272 <211> LENGTH: 30	
273 <212> TYPE: DNA	
274 <213> ORGANISM: Artificial Sequence	
276 <220> FEATURE:	
277 <223> OTHER INFORMATION: Primer	
279 <400> SEQUENCE: 25	30
280 cccttaatta atatacagat ctcaacggat 282 <210> SEQ ID NO: 26	30
283 <211> LENGTH: 31	
284 <212> TYPE: DNA	
285 <213> ORGANISM: Artificial Sequence	
287 <220> FEATURE:	
288 <223> OTHER INFORMATION: Primer	
290 <400> SEQUENCE: 26	
291 ccatcgataa tggccttcta caaagataac c	31
293 <210> SEQ ID NO: 27	
294 <211> LENGTH: 33	
295 <212> TYPE: DNA	
296 <213> ORGANISM: Artificial Sequence	
298 <220> FEATURE:	
299 <223> OTHER INFORMATION: Primer 301 <400> SEQUENCE: 27	
302 ccatcgataa tgagccatcc caagggaagt agg	33
304 <210> SEQ ID NO: 28	
305 <211> LENGTH: 33	
306 <212> TYPE: DNA	
307 <213> ORGANISM: Artificial Sequence	
309 <220> FEATURE:	
310 <223> OTHER INFORMATION: Primer	
312 <400> SEQUENCE: 28	
313 ccatcgataa tgaacagaga acatcttatg att	33
315 <210> SEQ ID NO: 29	
316 <211> LENGTH: 29	
317 <212> TYPE: DNA	
318 <213> ORGANISM: Artificial Sequence	
320 <220> FEATURE:	
321 <223> OTHER INFORMATION: Primer	
323 <400> SEQUENCE: 29	

RAW SEQUENCE LISTING ERROR SUMMARY

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003 TIME: 16:31:44

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\1667947.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 2

Seq#:35; Xaa Pos. 5,6,7

Seq#:36; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,15,16,17,20

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003 TIME: 16:31:44

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0 L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35 L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35 L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0 $L:418\ M:258\ W:$ Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:422 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:426 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:430 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:434 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:438 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:442 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:446 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:450 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:454 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:458 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:462 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:466 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36 L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0